

# SEQUENCE LISTING



<110> AMANO ENZYME INC.  
Takeuchi, Ken-Ichi  
Isobe, Kimiyasu  
Moriguchi, Mitsuaki  
Hirose, Yoshihiko  
Koide, Yoshinao

<120> TRANSFORMED MICROORGANISM AND PROCESS FOR PRODUCING D-AMINOACYLASE

<130> 217301US-0

<140> 10/009,782

<141> 2002-03-25

<150> PCT/JP00/03932

<151> 2000-06-15

<150> JAPAN 11/170555

<151> 1999-06-17

<160> 3

c2 <170> PatentIn version 3.1

<210> 1

<211> 1758

<212> DNA

<213> Alcaligenes xylosoxydans subsp. xylosoxydans

<220>

<221> CDS

<222> (34)..(1485)

<223>

<400> 1

gaattccact	tgatcgcgga	aggagagatt	tcc	atg	tcc	caa	tcc	gat	tcc	cag	54
				Met	Ser	Gln	Ser	Asp	Ser	Gln	
			1					5			

ccc	ttc	gac	ctg	ctg	ctc	gcg	ggc	ggc	acc	ctc	atc	gac	ggc	agc	aac	102
Pro	Phe	Asp	Leu	Leu	Leu	Ala	Gly	Gly	Thr	Leu	Ile	Asp	Gly	Ser	Asn	
		10					15					20				

acc	ccg	ggg	cgg	cgc	gcc	gac	ctg	ggc	gtg	cgc	ggc	gac	cgc	atc	gcc	150
Thr	Pro	Gly	Arg	Arg	Ala	Asp	Leu	Gly	Val	Arg	Gly	Asp	Arg	Ile	Ala	
	25				30					35						

gcc	atc	ggc	gat	ctg	tcg	gac	gcc	gcc	gcg	cac	acc	cgg	gtc	gac	gtg	198
Ala	Ile	Gly	Asp	Leu	Ser	Asp	Ala	Ala	Ala	His	Thr	Arg	Val	Asp	Val	
40					45					50				55		

tcg	ggc	ctg	gtg	gtc	gcg	ccc	ggc	ttc	atc	gac	tcg	cac	acc	cac	gac	246
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

RECEIVED

MAY 27 2003

TECH CENTER 1600/2900

Ser	Gly	Leu	Val	Val	Ala	Pro	Gly	Phe	Ile	Asp	Ser	His	Thr	His	Asp	
				60					65					70		
gac	aac	tac	ctg	ctc	agg	cgt	cgc	gac	atg	acg	ccc	aag	atc	tcg	cag	294
Asp	Asn	Tyr	Leu	Leu	Arg	Arg	Arg	Asp	Met	Thr	Pro	Lys	Ile	Ser	Gln	
			75					80					85			
ggc	gtc	acc	acg	gtg	gtc	acg	ggc	aat	tgc	ggc	atc	agc	ctg	gcg	ccg	342
Gly	Val	Thr	Thr	Val	Val	Thr	Gly	Asn	Cys	Gly	Ile	Ser	Leu	Ala	Pro	
		90					95					100				
ctg	gcg	cac	gcc	aac	ccg	ccc	gcc	ccc	ctg	gac	ctg	ctg	gac	gaa	ggc	390
Leu	Ala	His	Ala	Asn	Pro	Pro	Ala	Pro	Leu	Asp	Leu	Leu	Asp	Glu	Gly	
	105					110					115					
ggc	tct	tac	cgt	ttc	gag	cgc	ttc	gcc	gac	tac	ctg	gac	gcg	ttg	cgg	438
Gly	Ser	Tyr	Arg	Phe	Glu	Arg	Phe	Ala	Asp	Tyr	Leu	Asp	Ala	Leu	Arg	
120					125					130					135	
gcc	acg	ccg	gcg	gcc	gtc	aac	gcc	gcc	tgt	atg	gtg	ggc	cat	tca	acg	486
Ala	Thr	Pro	Ala	Ala	Val	Asn	Ala	Ala	Cys	Met	Val	Gly	His	Ser	Thr	
				140					145					150		
ctg	cgc	gcc	gcg	gtc	atg	ccg	gac	ttg	cag	cgc	gcc	gcc	acc	gac	gag	534
Leu	Arg	Ala	Ala	Val	Met	Pro	Asp	Leu	Gln	Arg	Ala	Ala	Thr	Asp	Glu	
			155					160					165			
gaa	atc	gcg	gcc	atg	cgg	gac	ctg	gcc	gag	gaa	gcc	atg	gcc	agc	ggc	582
Glu	Ile	Ala	Ala	Met	Arg	Asp	Leu	Ala	Glu	Glu	Ala	Met	Ala	Ser	Gly	
		170					175					180				
gcc	atc	ggc	att	tcg	acc	ggc	gcc	ttc	tac	ccg	ccc	gcc	gcc	cgc	gcc	630
Ala	Ile	Gly	Ile	Ser	Thr	Gly	Ala	Phe	Tyr	Pro	Pro	Ala	Ala	Arg	Ala	
	185					190					195					
acc	acc	gaa	gag	atc	atc	gag	gtg	tgc	cgg	ccg	ctg	agc	gcg	cat	ggc	678
Thr	Thr	Glu	Glu	Ile	Ile	Glu	Val	Cys	Arg	Pro	Leu	Ser	Ala	His	Gly	
200					205					210					215	
ggc	atc	tac	gcc	acc	cac	atg	cgc	gac	gaa	ggc	gag	cac	atc	gtg	gcc	726
Gly	Ile	Tyr	Ala	Thr	His	Met	Arg	Asp	Glu	Gly	Glu	His	Ile	Val	Ala	
				220					225					230		
gcg	ctg	gag	gaa	acc	ttc	cgc	atc	ggc	cgc	gag	ctg	gac	gtg	ccg	gtg	774
Ala	Leu	Glu	Glu	Thr	Phe	Arg	Ile	Gly	Arg	Glu	Leu	Asp	Val	Pro	Val	
			235					240					245			
gtg	atc	tcg	cac	cac	aag	gtc	atg	ggc	cag	ccc	aat	ttc	ggc	cgc	tcg	822
Val	Ile	Ser	His	His	Lys	Val	Met	Gly	Gln	Pro	Asn	Phe	Gly	Arg	Ser	
		250					255					260				
cgc	gag	acg	ctg	ccg	ctg	atc	gag	gcc	gcc	atg	gcg	cgc	cag	gac	gtc	870

Arg	Glu	Thr	Leu	Pro	Leu	Ile	Glu	Ala	Ala	Met	Ala	Arg	Gln	Asp	Val	
265						270					275					
tcg	ctg	gac	gcg	tat	ccc	tac	gtg	gcc	ggc	tcc	acc	atg	ctc	aag	cag	918
Ser	Leu	Asp	Ala	Tyr	Pro	Tyr	Val	Ala	Gly	Ser	Thr	Met	Leu	Lys	Gln	
280					285					290					295	
gac	cgc	gtg	ctg	ctg	gcc	gga	cgc	acc	atc	atc	acc	tgg	tgc	aag	ccc	966
Asp	Arg	Val	Leu	Leu	Ala	Gly	Arg	Thr	Ile	Ile	Thr	Trp	Cys	Lys	Pro	
				300					305					310		
ttc	ccc	gaa	ctg	agc	ggg	cgc	gac	ctg	gat	gaa	gtc	gcg	gcc	gag	cgc	1014
Phe	Pro	Glu	Leu	Ser	Gly	Arg	Asp	Leu	Asp	Glu	Val	Ala	Ala	Glu	Arg	
			315					320					325			
ggc	aaa	tcc	aag	tac	gac	gtg	gtg	ccc	gag	ctg	cag	ccg	gcc	ggc	gcc	1062
Gly	Lys	Ser	Lys	Tyr	Asp	Val	Val	Pro	Glu	Leu	Gln	Pro	Ala	Gly	Ala	
		330					335					340				
atc	tac	ttc	atg	atg	gac	gaa	ccc	gac	gtg	cag	cgc	atc	ctg	gcg	ttc	1110
Ile	Tyr	Phe	Met	Met	Asp	Glu	Pro	Asp	Val	Gln	Arg	Ile	Leu	Ala	Phe	
	345					350					355					
ggc	ccg	acc	atg	atc	ggc	tcc	gac	ggc	ctg	ccg	cac	gac	gag	cgc	ccg	1158
Gly	Pro	Thr	Met	Ile	Gly	Ser	Asp	Gly	Leu	Pro	His	Asp	Glu	Arg	Pro	
360					365					370					375	
cat	ccg	cgc	ctg	tgg	ggc	acc	ttc	ccg	cgg	gtg	ctg	ggg	cac	tat	gcg	1206
His	Pro	Arg	Leu	Trp	Gly	Thr	Phe	Pro	Arg	Val	Leu	Gly	His	Tyr	Ala	
				380					385					390		
cgc	gac	ctg	ggc	ctg	ttc	ccg	ctg	gag	acg	gcg	gta	tgg	aag	atg	acc	1254
Arg	Asp	Leu	Gly	Leu	Phe	Pro	Leu	Glu	Thr	Ala	Val	Trp	Lys	Met	Thr	
			395					400					405			
ggc	ctg	acc	gcc	gcg	cgc	ttc	ggc	ctg	gcc	ggg	cgc	ggg	cag	ctg	cag	1302
Gly	Leu	Thr	Ala	Ala	Arg	Phe	Gly	Leu	Ala	Gly	Arg	Gly	Gln	Leu	Gln	
		410					415					420				
gcc	ggg	tac	ttc	gcc	gac	ctg	gtg	gtg	ttc	gac	ccg	gcc	acg	gtg	gcc	1350
Ala	Gly	Tyr	Phe	Ala	Asp	Leu	Val	Val	Phe	Asp	Pro	Ala	Thr	Val	Ala	
	425					430					435					
gat	acc	gcc	acc	ttc	gaa	cac	cct	acc	gag	cgc	gcc	gcc	ggc	atc	cat	1398
Asp	Thr	Ala	Thr	Phe	Glu	His	Pro	Thr	Glu	Arg	Ala	Ala	Gly	Ile	His	
440					445					450					455	
tcc	gtg	tac	gtc	aac	ggc	gcg	ccg	gtc	tgg	caa	gag	cag	gcg	ttc	acc	1446
Ser	Val	Tyr	Val	Asn	Gly	Ala	Pro	Val	Trp	Gln	Glu	Gln	Ala	Phe	Thr	
				460					465					470		
ggc	cag	cat	gcc	ggc	cgc	gtg	ctc	gca	cgc	acg	gcc	gcc	tgag	cccc	ggc	1495

Gly Gln His Ala Gly Arg Val Leu Ala Arg Thr Ala Ala  
 475 480

gccagccctt acaatccggc gtgaacgggg cggcgtgccg cccctccca accctggacg 1555  
 caaaccgcta catggcccct ccctccgctc gcaatacggc cccacccgat atcgtgggca 1615  
 aggaagtgat gggcgcgcg ctcgcgcgccg agcgcaaggc ccggaaaatg accctgcaag 1675  
 acctgtcgca ggccagcggc atcgcggtct cgaccctgtc caaggccgag ctggggccaga 1735  
 tcgccctgag ctacgagaag ctt 1758

<210> 2

<211> 484

<212> PRT

<213> Alcaligenes xylosoxydans subsp. xylosoxydans

<400> 2

Met Ser Gln Ser Asp Ser Gln Pro Phe Asp Leu Leu Leu Ala Gly Gly  
 1 5 10 15

Thr Leu Ile Asp Gly Ser Asn Thr Pro Gly Arg Arg Ala Asp Leu Gly  
 20 25 30

Val Arg Gly Asp Arg Ile Ala Ala Ile Gly Asp Leu Ser Asp Ala Ala  
 35 40 45

Ala His Thr Arg Val Asp Val Ser Gly Leu Val Val Ala Pro Gly Phe  
 50 55 60

Ile Asp Ser His Thr His Asp Asp Asn Tyr Leu Leu Arg Arg Arg Asp  
 65 70 75 80

Met Thr Pro Lys Ile Ser Gln Gly Val Thr Thr Val Val Thr Gly Asn  
 85 90 95

Cys Gly Ile Ser Leu Ala Pro Leu Ala His Ala Asn Pro Pro Ala Pro  
 100 105 110

Leu Asp Leu Leu Asp Glu Gly Gly Ser Tyr Arg Phe Glu Arg Phe Ala  
 115 120 125

Asp Tyr Leu Asp Ala Leu Arg Ala Thr Pro Ala Ala Val Asn Ala Ala  
130 135 140

Cys Met Val Gly His Ser Thr Leu Arg Ala Ala Val Met Pro Asp Leu  
145 150 155 160

Gln Arg Ala Ala Thr Asp Glu Glu Ile Ala Ala Met Arg Asp Leu Ala  
165 170 175

Glu Glu Ala Met Ala Ser Gly Ala Ile Gly Ile Ser Thr Gly Ala Phe  
180 185 190

Tyr Pro Pro Ala Ala Arg Ala Thr Thr Glu Glu Ile Ile Glu Val Cys  
195 200 205

Arg Pro Leu Ser Ala His Gly Gly Ile Tyr Ala Thr His Met Arg Asp  
210 215 220

Glu Gly Glu His Ile Val Ala Ala Leu Glu Glu Thr Phe Arg Ile Gly  
225 230 235 240

Arg Glu Leu Asp Val Pro Val Val Ile Ser His His Lys Val Met Gly  
245 250 255

Gln Pro Asn Phe Gly Arg Ser Arg Glu Thr Leu Pro Leu Ile Glu Ala  
260 265 270

Ala Met Ala Arg Gln Asp Val Ser Leu Asp Ala Tyr Pro Tyr Val Ala  
275 280 285

Gly Ser Thr Met Leu Lys Gln Asp Arg Val Leu Leu Ala Gly Arg Thr  
290 295 300

Ile Ile Thr Trp Cys Lys Pro Phe Pro Glu Leu Ser Gly Arg Asp Leu  
305 310 315 320

Asp Glu Val Ala Ala Glu Arg Gly Lys Ser Lys Tyr Asp Val Val Pro  
325 330 335

Glu Leu Gln Pro Ala Gly Ala Ile Tyr Phe Met Met Asp Glu Pro Asp  
340 345 350

Val Gln Arg Ile Leu Ala Phe Gly Pro Thr Met Ile Gly Ser Asp Gly  
355 360 365

Leu Pro His Asp Glu Arg Pro His Pro Arg Leu Trp Gly Thr Phe Pro  
370 375 380

Arg Val Leu Gly His Tyr Ala Arg Asp Leu Gly Leu Phe Pro Leu Glu  
385 390 395 400

Thr Ala Val Trp Lys Met Thr Gly Leu Thr Ala Ala Arg Phe Gly Leu  
405 410 415

Ala Gly Arg Gly Gln Leu Gln Ala Gly Tyr Phe Ala Asp Leu Val Val  
420 425 430

Phe Asp Pro Ala Thr Val Ala Asp Thr Ala Thr Phe Glu His Pro Thr  
435 440 445

Glu Arg Ala Ala Gly Ile His Ser Val Tyr Val Asn Gly Ala Pro Val  
450 455 460

Trp Gln Glu Gln Ala Phe Thr Gly Gln His Ala Gly Arg Val Leu Ala  
465 470 475 480

Arg Thr Ala Ala

<210> 3  
<211> 6  
<212> DNA  
<213> Artificial

<220>

<223> Nucleotide sequence in ribosome binding site for improving translation efficiency.

<400> 3  
gaagga